EXHIBIT D:

COMPARISON OF RAT AND HUMAN LKB1

BLAST

Basic Local Alignment Search Tool

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

SEQ ID NO: 6

Results for: |cl|17777 SEQ ID NO: 6(433aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

<u>lc({17777</u> Icl]17777

Description

SEQ ID NO: 6

Molecule type

amino acid

Query Length

433

Subject ID

gi|157820995|ref|NP_001101539.1|

Description

serine/threonine-protein kinase 11 [Rattus norvegicus] >gi|149034596|gb|EDL89333.1| serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus norvegicus]

Molecule type

amino acid

Subject Length

436

Program

BLASTP 2.2.24+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: Search Summary [Taxonomy reports] [Multiple alignment]

Search Parameters

Search parameter name Search parameter value

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hitlist size	100
Gapcosts:	11,1
Matrix	BLOSUM62

Low Complexity Filter	Yes	
Filter string	L;	
Genetic Code	1 .	
Window Size	40	
Threshold	11	
Composition-based stats	2	

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320459	0.267
K	0.139595	0.041
Н	0.429592	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

Effective search space

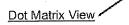
110297

Graphic Summary

Distribution of Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Plot of IcI|17777 vs gi|157820995|ref|NP_001101539.1| [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

				Score	· <u>E</u>
Sequences producing	significant alignments:			(Bits)	Value
ref NP 001101539.1	serine/threonine-protein kind	ase 11	[Rattu	525	1e-153

<u>Alignments</u>

>ref|NP 001101539.1| serine/threonine-protein kinase 11 [Rattus norvegicus]
 gb|EDL89333.1| serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus
norvegicus]
Length=436

```
Score = 525 bits (1351), Expect = 1e-153, Method: Compositional matrix adjust. Identities = 287/300 (96%), Positives = 291/300 (97%), Gaps = 0/300 (0%)
              KLIGKYLMGDLLGEGSYGKVKEVLDSETLCRRAVkilkkklrriPNGEANVKKEIQLLR
                                                                                          103
Ouerv
              KLIGKYLMGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKKLRRIPNGEANVKKEIQLLR
              KLIGKYLMGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKKLRRIPNGEANVKKEIQLLR
Sbjet
              RLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPVCQAHGYFCQLIDG
        104
                                                                                          163
Query
              RLRH+NVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPVCQAHGYF QLIDG
                                                                                          163
              RLRHRNVIÖLVDVLYNEEKOKMYMVMEYCVCGMQEMLDSVPEKRFPVCQAHGYFRQLIDG
        104
Sbjct
              LEYLHSQGIVHKDIKPGnlllttggtlKISDLGVAEALHPFAADDTCRTSQGSPAFQPPE
LEYLHSQGIVHKDIKPGNLLLTT GTLKISDLGVAEALHPFA DDTCRTSQGSPAFQPPE
                                                                                          223
Query
        164
              LEYLHSQGIVHKDIKPGNLLLTTNGTLKISDLGVAEALHPFAVDDTCRTSQGSPAFQPPE
                                                                                          223
Sbjct
        164
                                                                                          283
              IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGKGSYAIPGDCGPPLS
        224
Query
              IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIG+G + IP DC PPLS
              IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGRGDFTIPCDCAPPLS
                                                                                          283
Sbjct
        224
              DLLKGMLEYEPAKRFSIRQIRQHSWFRKKHPPAeeapvpippspDTKDRWRSMTVVPYLEDDLL+GMLEYEPAKRFSIRQIRQHSWFRKKHPAEAVPIPPSPDTKDRWRSMTVVPYLED
Query
        284
              DLLRGMLEYEPAKRFSIRQIRQHSWFRKKHPLAEALVPIPPSPDTKDRWRSMTVVPYLED
Sbjct
        284
```